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in which contamination is rare. This kind of sporadic contamination is especially problematic in an extremely large throughput assay in which 5 to 10 negative controls are run for approximately every 1000 samples. Statistically, the likelihood of sporadic contamination in, for example, 1000 samples will not be detected in only 5 negative controls. Sporadic contamination is also a significant problem when PCR based analyses are performed on heterogeneous (rare event analysis) samples in which a positive result is generated from, for example, 1-5% of the total amplification product present within the sample. Generally, within a PCR based inherited disease diagnostic assay, given the 50% heterogeneity that exists in any genomic DNA sample, a 1-5% increase in signal in a true negative sample would appear as a slight increase in background, but would not indicate a false positive result. However, within an assay involving samples with heterogeneous populations of DNA, a 1-5% positive signal generated by a true negative sample would result in a false positive.

On page 4, please delete the paragraph starting on line 6 and ending on line 23, and substitute the following therefor:

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In a preferred embodiment, the amplification reaction is selected from PCR, reverse transcriptase PCR, and quantitative PCR. Also in a preferred embodiment, the sample containing nucleic acid to be amplified is a stool sample. A stool sample contains a highly-heterogeneous population of nucleic acids. Human nucleic acids represent a small portion of the nucleic acid present in stool. More specifically, a stool sample may contain molecular indicia of cancer, specifically colorectal cancer, that occurs as a small subpopulation (typically on the order of about 1% at early stages of cancer or precancer) of the total nucleic acid in the stool. Sensitive assays (which may or may not involve amplification) have been developed to detect such small subpopulations. See, e.g., U.S. Patent No. 5,670,325, incorporated by reference herein. Amplification of